

human neutral Sphingomyelinase (NSM) Gene Sequence

ACCGCGGCCGTCGCTGGAGAGTTGAGCCGCCTAGCGCCCTGGAGCTCCCCAACCATGA 60
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TGCGCGCCGGCAGCGACCTCTCAAGCTCGGCGGATCGCGGGGACCTCGAGGGGTGGTACT 60
E I
AGCCCAACTTCTCCCTGCGACTGCGGATCTTCAACCTCAACTGCTGGTGAGTGCGTCTGC 120
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCGGGTGAAGAGGGACGCTGACGCCTAGAAGTTGGAGTTGACGACCACTCACGCAGACG 120
GGAGTGGGGTCTGGGGGCCACCTTCCGTTGCGACCCATGCAGCCTTCCTCCCCCTATCCC 180
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CCTCACGCCAGACCCCGGTGGAAGCAAGCGTGGGTACGTCGGAGGAGGGGGATAGGG 180
GCCCCACGATCTCAGGGTGTAGGGAACCCGAACCTCCAAAGTCCACATCTGGCCCCAG 240
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CGGGGTGCTAGAGTCCCACATCCCTTTTGGGCTTGGAGGTTTCAGGTGTAGACCGGGGTC 240
CGCCGGTGGTCCCAGCAGTCGCCTCCCCTGCCCGCTCTTCCCTTCCTTAGGGGCATTCC 300
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCGGCCACCAGGTCGTCAGCGGAGGGGACGGGCGGAGAAGGAATCCCCGTAAGG 300
GTACTTGAGCAAGCACCAGGCGGACCGCATGAGGCGCCTGGGAGACTTCTGAACCAGGA 360
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CATGAACCTCGTTCGTGGCCCGGCTGGCGTACTCCGCGGACCTCTGAAAGACTTGGTCCT 360
E II
GAGCTTCGACCTGGCTTTGCTGGAGGAGGTGAGATTGTGCAGCACGGTGCGGAACCCAGG 420
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CTCGAAGCTGGACCGAAACGACCTCCTCCACTTAACACGTCGTGCCACGCCTTGGGTCC 420
CTGGGAGGAGGGACAGACCGTCCCCTGGGGAAGACCAAGCAGGCATCCTCACCGCTTC 480
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GACCCCTCCTCCCTGTCTGGCAGGGTGACCCCTTCTGGTTCGTCCGTAGGAGTGGCGAAG 480
CCTCAGGTGTGGAGTGAGCAGGACTTCCAGTACCTGAGACAGAAGCTGTACCTACCTAC 540
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGAGTCCACACCTCACTCGTCCTGAAGGTCATGGACTCTGTCTCGACAGTGGATGGATG 540
E III
CCAGCTGCACACCACTTCCGGAGGTGAGAAGCCCACTGGCCTGAAGCCTGTTGTATCCC 600
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGTCGACGTGTGGTGAAGGCTCCACTCTTCGGGTGACCGGACTTCGGACACAGTAGGG 600
AGGAGGCTCTTGCCCTGCCAGCCCTTCCCTATCCTGCCTGCACTCTCCAGTCTCCTCCA 660
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCCGAGAACCAGGACGGTCGGAAGGGATAGGACGGACGTGAGAGGTCAGAGGAGGT 660
GCCTCCTCTCCCTCTGGATGTGAGAGAAGGAGAAGGGTGAACCAAGAAGGTCCTATGACT 720
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CGGAGGAGAGGGAGACCTACACTCTCTTCCCTCTCCACTTGGTTCTTCCAGGATACTGA 720
TCAGCCCATTTTCAGCTTTGTTTTCTGGCTGCCCTATACTCCTCCAAAGGCCGTCGCCTTG 780
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
AGTCGGGTAAAGTCGAAACAAAAGACCGACGGGATATGAGGAGGTTTCCGGCAGCGGAAC 780
GTTCTAGGGCTAGTCCCAGCAGTAGAAAAAGAAAAAATAGCTGATCAGAGCTGGAAGAC 840
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CAAGATCCCAGTACAGGGTCGTATCTTTTTCTTTTTTATCGACTAGTCTCGACCTTCTG 840
AAGGGAGGGGAAGAAGGCTGGGTGTCTCTCCCTGTTTTTCTGGTTATTAAGCAGGGCTTG 900
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTCCCTCCCTTCTTCCGACCCACAGAGAGGGACAAAAAGACCAATATTTCGTCCCGAAC 900

Figure 1-1

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CTCTCCCTCCTTCTCCCCACATCCTAGCATGAGCCAATGATTCCCTTAGGGCTCTGAGG
 1861 -----+-----+-----+-----+-----+ 1920
 GAGAGGGAGGAAGAGGGGGTGTAGGATCGTACTCGGTTACTAAGGGAATCCCGAGACTCC
 AAGGCAACACAATGGTACCCAAGAAGTACGTACGCCAGCAGGAGCTGAAGCCATTTC
 1921 -----+-----+-----+-----+-----+ 1980
 TTCCGTTGTGTTACCATGGGTTCTTGACNATGCAGTCGGTCGTCTCGACTTCGGTAAAG
 CCTTTGGTGTCGCGATTGACTACGTGCTTTACAAGGTCAGGCTCCTCCCTTCAACATGCT
 1981 -----+-----+-----+-----+-----+ 2040
 GGAAACCACAGGCGTAAGTATGCACGAAATGTTCCAGTCCGAGGAGGGAAGTTGTACGA
 TTCATATGCTGTGTCTCTTTGTCTACTAACCTGTGTAGATCCTTTGCTCAGNTAGTCTAG
 2041 -----+-----+-----+-----+-----+ 2100
 AAGTATACGACACAGAGAAACAGATGATTGGACACATCTAGGAAACGAGTCNATCAGATC
 TCTTGGACCACTGATGGGTGGAAAGTGGGGTAGCCGGGAGCTGGTTCTCTGGGAAGAGGC
 2101 -----+-----+-----+-----+-----+ 2160
 AGAACCTGGTGACTACCCACCTTTCACCCCATCGGCCCTCGACCAAGAGACCCCTCTCCG
 CCTCATATATAAGCTTCTCTNTGGCCCTTACTTTTCTAGGCAGTTTCTGGGTTTACAT
 2161 -----+-----+-----+-----+-----+ 2220
 GGAGTATATATTGAAAGAGANACCGGAATGAAAAGGATCCGTCAAAGACCCAAAATGTA
 CTCCTGTAAGAGTTTGAACCACCTACAGGCTTTGACCCTNACAGGGGCACCCCCCTCTC
 2221 -----+-----+-----+-----+-----+ 2280
 GAGGACATTCTCAAACCTTGGTGATGTCCGAACTGGGANTGTCCCCGTGGGGGAGAG
 TTGATCATGAAGCCCTGATGGCTACTCTGTTTGTGAGGCACAGCCCCACAGCAGAACC
 2281 -----+-----+-----+-----+-----+ 2340
 AACTAGTACTTCGGGACTACCGATGAGACAAACACTCCGTGTCGGGGGTGTCTGCTTGG
 CCAGCTCTACCCACGGTGAGTCACCCCCACCTTTCTTGGCCCTTGCCCCGCTTGAAGC
 2341 -----+-----+-----+-----+-----+ 2400
 GGTGAGATGGGTCCCACTCAGTGGGGGTGGGAAAGGAACCGGGAACGGGGCGAATTTCG
 AGCCCTTCCACTCTTGACTCTCTCTGCCCCACTGCCTGCTCTGTTGTAGGACCAGCAG
 2401 -----+-----+-----+-----+-----+ 2460
 TCGGGAAGGTGAGAACTGAGAGAGGACGGGGTGACGGGACGAGACAACATCCTGGTCGTC
 AGAGGTGCGCGTTGATGTGTGTGCTAAAGGAGGCTGGAAGGAGCTGGGTCTGGGCATGG
 2461 -----+-----+-----+-----+-----+ 2520
 TCTCCAGCGGCAACTACACACAGATTTCCTCCGACCTGCCTCGACCCAGACCCGTACC
 CTCAGGCTCGCTGGTGGGCCACCTTCGCTAGCTATGTGATTGGCCTGGGGCTGCTTCTCC
 2521 -----+-----+-----+-----+-----+ 2580
 GAGTCCGAGCGACACCCCGGTGGAAGCGATCGATACACTAACCGGACCCCGACGAAGAGG
 TGGCACTGCTGTGTCTCTGGCGGCTGGAGGAGGGCCGGGAAGCTGCCATACTGCTCT
 2581 -----+-----+-----+-----+-----+ 2640
 ACCGTGACGACACACAGGACCGCCGACCTCCTCCCGGCCCTTCGACGGTATGACGAGA
 GGACCCCCAGTGTAGGGCTGGTGCTGTGGGCAGGTGCATTCTACCTCTTCCACGTACAGG
 2641 -----+-----+-----+-----+-----+ 2700
 CCTGGGGGTACATCCCGACACGACACCCGTCCACGTAAGATGGAGAAGGTGCATGTCC
 AGGTCAATGGCTTATATAGGGCCAGGCTGAGCTCCAGCATGTGCTAGGAAGGGCAAGGG
 2701 -----+-----+-----+-----+-----+ 2760
 TCCAGTTACCGAATATATCCCGGTCCGACTCGAGGTCGTACACGATCCTTCCCGTTCCC
 AGGCCAGGATCTGGGGCCAGAGCCTACGCCAGCCCTACTCCTGGGGCAGCAGGAGGGGG
 2761 -----+-----+-----+-----+-----+ 2820
 TCCGGGTCTAGACCCGGGTCTCGGAGTCGGTCGGGATGAGGACCCCGTCGTCTCCCC
 ACAGAACTAAAGAACAATAAAGCTTGGCCCAA

E VIII

E IX

E X

Figure 1-2

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2821 -----+-----+-----+----- 2852
TGTCTTGATTTCCTTGTTATTTCGAACCGGGTT

Figure 1-3

Mouse Neutral Sphingomyelinase (nSMase) gene sequence

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TNGANNCTGTTAGCTCCAGNCCGGTNGGTCGCCGTNCTAGNCNNATCTNTATAGCTCTTC
1  -----+-----+-----+-----+-----+-----+ 60
ANCTNNGACAATCGAGGTCNGGCCANCCAGCGGCANGATCNGNNTAGANATATCGAGAAG

GTTGCGAGCNCAATTNNNTCTCAATAAANGGATNCANCCCTATGACAGAACGTGGACCCC
61  -----+-----+-----+-----+-----+-----+ 120
CAACGCTCGNGTTAANNNAGAGTTATTTNCCTANGTNGGGATACTGTCTTGACCTGGGG

CGCCCGCCANCNCANGNGANACCGCGGCATGGGNCTGAGGTGCNCANGGTGTCTGGGGCG
121  -----+-----+-----+-----+-----+-----+ 180
GCGGGCGGTNGGTNCTNTGGCGCCGTACCCNGACTCCACGNGTNCCACAGACCCCGC

AGGGGTTACCTCAGCGATGGTCTTTGACACCTGAAAGCTGGAGCTTTTGAANAGCCCCAN
181  -----+-----+-----+-----+-----+-----+ 240
TCCCCAATGGAGTCGCTACCAGAACTGTGGACTTTCGACCTCGAAAACCTTNTCGGGGTN

CACCTTCAGCTTCAGGGGCGGCTCNGGCGGCAACCGCACGTGANATGCTGGGGGCTTCGA
241  -----+-----+-----+-----+-----+-----+ 300
GTGGAAGTCGAAGTCCCCGCGAGNCCGCGTGGCGTGCACNTACGACCCCGAAGCT

CTTGGGCCGGCACGGNTGCTGGGTGGCCATGGAANNACAGNACAGAGCCCGGNACACAA
301  -----+-----+-----+-----+-----+-----+ 360
GAACCCGGCCGTGCCNACGACCCACCGGTACCTTNNNTGTCNTGTCTCGGGCCNTGTGTT

ATANTGCGAGTCGCCANGGNAACCGCGTGGCTCCTCCCCGAACGCCCNCAAGGGGCGGGA
361  -----+-----+-----+-----+-----+-----+ 420
TATNACGCTCAGCGGTNCCNTTGGCGCACCGAGGAGGGGCTTGCGGGNGTTCCCCGCCCT

CCTGAGTGAGTTCTNTGGGCGGGGCTCNCATCAACTTCAAGCCTGTTGCTGGTGGAAGCC
421  -----+-----+-----+-----+-----+-----+ 480
GGACTCACTCAAGNACCCGCCCGGAGNGTAGTTGAAGTTCGGACAACGACCACCTTCGG

GAGCCGGGAACAAGGGAGGAACCTGTAGGCCGCGGTGCGGATAACCCACCGAAGGACCTA
EI 481 -----+-----+-----+-----+-----+-----+ 540
CTCGGCCCTTGTTCCCTCCTTGGACATCCGGCGCCACGCCTATTGGGTGGCTTCCTGGAT

AGAATCTGGAACAGTCCACCCGAGATTCTTCCAGGACTGCCGGCGGACTCTCGCATTC
541  -----+-----+-----+-----+-----+-----+ 600
TCTTAGACCTTGTCAGGTGGGCTCTAAGGAAGGTCTGACGGCCGCTGAGAGCGTAAGT

GCCCGGGATTGTCAGCCGACCTTCTTTCCGGGTGGAATGACGGCCTTTGTCCCAGTAACG
601  -----+-----+-----+-----+-----+-----+ 660
CGGGCCCTAAACGTCGGCTGGAAGAAAGGCCACCTTACTGCCGGAACAGGGTCATTGC

CAGGAGTCNNCCCCACCCCAACCAGCTCGCGTTCCTGGGTGCGGGCAGCGCAGGATAGG
661  -----+-----+-----+-----+-----+-----+ 720
GTCCTCAGNNGGGGTGGGGTTGGTCGAGCGCAAGGACCCAGCCCCGTGCGTCTATCC
GCAATAAGCCTGTGCGCGCAATCCGCCTCGCCGCCCTTGCTCCGAAGCACTCCAGCCATG
721  -----+-----+-----+-----+-----+-----+ 780
CGTTATTTCGGACACGCGCGTTAGGCGGAGCGGCGGGAACGAGGCTTCGTGAGGTTCGGTAC
AAGCTCAACTTTTCTCTACGCTGAGAGTTTCAATCTCAACTGCTGgtaagtaagtgc
781  -----+-----+-----+-----+-----+-----+ 840
TTCGAGTTGAAAAGAGATGCCGACTCTCAAAAGTTAGAGTTGACGACcattcattcacga

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Figure 2-1

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ccccaggcgtgggCTGCAGCCTCGGAGCCACCTTCCAGTCCCCTCTCGCACATGCCTAGGA
841 -----+-----+-----+-----+-----+ 900
gggtccgcacccGACGTCGGAGCCTCGGTGGAAGGTCAGGGGAGAGCGTGTACGGATCCT

AGGAAGCAGGTCTTCTTCAGCCGAGCTAGACCCCTGTCCTTCCCGAACCACCAAAGTCCAC
901 -----+-----+-----+-----+-----+ 960
TCCTTCGTCCAGAAGAAGTCGGCTCGATCTGGGACAGGAAGGGCTTGGTGGTTTCAGGTG

ATCGCCTAAAGACCAGAGCTTGGGTGGTTGCAGCAATCACCAAAGTCCCTATCATCCAAA
961 -----+-----+-----+-----+-----+ 1020
TAGCGGATTTCTGGTCTCGAACCCACCAACGTCGTTAGTGGTTTCAGGGATAGTAGGTTT

GCTGAGGTGATGACAGCAGTAATCGTCCCAACCTGGCCCATGTCTTTCCTTTTAAATGA
1021 -----+-----+-----+-----+-----+ 1080
CGACTCCACTACTGTCTCATTAAGCAGGGTTTGGACCGGGTACAGAAAGGAAAATTTACT

TTTACTTTTATTTTATGTACATTTGGTGTTTTGCCCTGTATGTATGTCTGTGTGAAGGTGC
1081 -----+-----+-----+-----+-----+ 1140
AAATGAAAATAAAAATACATGTAAACCACAAAACGGACATACATACAGACACACTTCCACG

CAGATTCTCTGGAAGTGGAGTTACAGACAGTTGTAAGCTGTCTATGTCTGTGTGAAGGTGC
1141 -----+-----+-----+-----+-----+ 1200
GTCTAAGAGACCTTGACCTCAATGTCTGTCAACATTCGACAGTACACGAACGACCTTTAA

GAACTGCTGACCCATCTCTTCTGCCCCCTGCGTCCCTCCACCCCTTTAGGGACATCCCCT
1201 -----+-----+-----+-----+-----+ 1260
CTTGACGACTGGGTAGAGAAGACGGGGGACGAGGAGGTGGGGAAAATCCCTGTAGGGGA

ACCTGAGCAAAACATAGGGCGGACCGCATGAAGCGCTTGGGAGACTTTCTGAACTTGGAAA
1261 -----+-----+-----+-----+-----+ 1320
TGGACTCGTTTGTATCCCGCCTGGCGTACTTCGCGAACCCTCTGAAAGACTTGAACCTTT

E II
ACTTTGATCTGGCTCTCCTGGAGGAGGTGAGGTTGTAGGGCAGGCTAGGTTGGAGGAGGG
1321 -----+-----+-----+-----+-----+ 1380
TGAAACTAGACCGAGAGGACCTCCTCCACTCCAACATCCCGTCCGATCCAACCTCCTCCC

CAGCAGGCGGCAGGCGGCGGCAGGAAAACCTGTTCTGTCTTGGGATGAAATCCCAAGCAA
1381 -----+-----+-----+-----+-----+ 1440
GTCGTCCGCGCTCCGCGCCGTCCTTTTGAACAAGACAGAACCCTACTTTAGGGTTCGTT

GTATCCTCACCTTCTTCTCCAGGTGTGGAGTGAGCAGGACTTCCAGTACCTAAGGCCAA
1441 -----+-----+-----+-----+-----+ 1500
CATAGGAGTGGAAGAAGGAGGTCCACACCTCACTCGTCCTGAAGGGTCATGGATTCCGTT

E III
AGGCTATCGCTCACCTATCCAGATGCACACTACTTCAGAAGGTGAAAAGCCTGTGTTCTC
1501 -----+-----+-----+-----+-----+ 1560
TCCGATAGCGAGTGGATAGGTCTACGTGTGATGAAGTCTTCCACTTTTCGGACACAAGAG

AGCCTGTTCTCAGACGAGGAAGCTCTCCAACATTCTTGCTTGACCCCTCGATCTTCTTCC
1561 -----+-----+-----+-----+-----+ 1620
TCGGACAAGAGTCTGCTCCTTCGAGAGGTTGTAAGAACGAACGTGGGAGCTAGAAGAAGG

TCTGGGTGTGAGAAGAGCAGGCCGTCACCTCATCTTGCAAGGGCTGCTGTCTTAGGCTT
1621 -----+-----+-----+-----+-----+ 1680
AGACCCACACTCTTCTCGTCCGGCAGTGGGAGTAGAACGTTCCCGACGACAGAATCCGAA

TGTTCTGGGGTTGATCTTAGCAGTAGAGCTGGGAGACCGCGGAGGGGAAGAGGGCTGGCT
1681 -----+-----+-----+-----+-----+ 1740
ACAAGACCCCAACTAGAATCGTCATCTCGACCCTCTGGCGCCTCCCCTTCTCCCGACCGA

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Figure 2-2

GGGTACTCCCCTCCTTGCTCTTCTGGTTATTAAGCAAGAGTTGGTTTTTCAGCGGGATGAT
 1741 -----+-----+-----+-----+-----+ 1800
 CCCATGAGGGGAGGAACGAGAAGACCAATAATTTCGTTCTCAACCAAAAGTCGCCCTACTA

E IV

AGGCAGTGGCCTCTGTGTGTTCTCCAAACACCCCAATCCAGGAAATCTTCCAGCATGTCTA
 1801 -----+-----+-----+-----+-----+ 1860
 TCCGTCACCGGAGACACACAAGAGGTTTGTGGGTTAGGTCCTTTAGAAGGTCGTACAGAT

CAGTCTGAATGGTTACCCCTACATGGTAAGGATCTCTTCCCTATCCTTGCTAACACAGAC
 1861 -----+-----+-----+-----+-----+ 1920
 GTCAGACTTACCAATGGGGATGTACCATTCTAGAGAAGGGATAGGAACGATTGTGTCTG

TGGACGCAGCCTTCTGGGGCCTTGGCAGGAGGGTGTGAGTACCCTGAGTTTTTGTCTTC
 1921 -----+-----+-----+-----+-----+ 1980
 ACCTGCGTCGGAAGGACCCCGAACCCTCTCCACAGTCATGGGACTCAAAAACAGAAG

TCTTGCCCTGCAGTTCCATCATGGAGACTGGTCTGTGGGAAGTCTGTGGGGCTGCTGGTG
 1981 -----+-----+-----+-----+-----+ 2040
 AGAACGGACGTCAGGTTAGTACCTCTGACCAAGACACCCTTCAGACACCCCGACGACCAC

E V

CTCCGTCTAAGTGGACTGGTGCTCAATGCCTACGTGACTCATGTGAGTGGGGCTAGCCAG
 2041 -----+-----+-----+-----+-----+ 2100
 GAGGCAGATTCACTGACACGAGTTACGGATGCACTGAGTACACTCACCCCGATCGGTC

GCTTAGGCAGTGGGTCAAGCAGCCCAATGCTATGGTGGAGAAGAGACGCCACTAGTTAGT
 2101 -----+-----+-----+-----+-----+ 2160
 CGAATCCGTCACCCAGTTCGTCGGGTTACGATACCACCTCTTCTCTGCGGTGATCAATCA

TCTGCTGCCTGGGGATAAGGCATGGGATCAGAAGCTAGCATTTGGGCAAGGTTCACCCAT
 2161 -----+-----+-----+-----+-----+ 2220
 AGACGACGGACCCCTATTCCGTACCCTAGTCTTCGATCGTAACCCGTTCCAAGTGGGTAA

CCCTGTCACACTCTGCCATGTGACAGATGACAAGCTTGATTTCAGACAGCCTTCTCTTTGA
 2221 -----+-----+-----+-----+-----+ 2280
 GGGACAGTGTGAGACGGTACACTGTCTACTGTTTGAACCTAAGTCTGTGCGGAAGAGAACT

TTTCACCTATTCCACTTTAGCTACATGCTGAGTACAGCCGACAGAAGGACATCTACTTTG
 2281 -----+-----+-----+-----+-----+ 2340
 AAAGTGGATAAGGTGAAATCGATGTACGACTCATGTGCGGCTGTCTTCTGTAGATGAAC

E VI

CACACCGTGTGGCCCAAGCTTGGGAACTGGCCCAAGTTTCATCCAGTGTGTGAGCCTGGGCT
 2341 -----+-----+-----+-----+-----+ 2400
 GTGTGGCACACCGGGTTCGAACCCTTGACCGGGTCAAGTAGGTCACACACTCGGACCCGA

TGATGGGGGCTGTGGGGTGGGGACGGGGTTGAGGGATGNGNAANTTATCCTTGAAGAGGG
 2401 -----+-----+-----+-----+-----+ 2460
 ACTACCCCGACACCCACCCCTGCCCAACTCCCTACNCNTTNAATAGGAACCTCTCCC

CACATAATAAGGGAAGAATTTCTCTCTTGCCGCTCTTCCCCCAACTCAGCCACACATCCA
 2461 -----+-----+-----+-----+-----+ 2520
 GTGTATTATTCCTTCTTAAAGGAGGAACGCGAGAAGGGGTTGAGTCGGTGTGTAGGT

E VII

AGAATGCAGATGTGGTTCTATTGTGTGGAGACCTCAATATGCACCCCAAAGACCTGGGCT
 2521 -----+-----+-----+-----+-----+ 2580
 TCTTACGTCTACACCAAGATAACACACCTCTGGAGTTATACGTGGGGTTTCTGGACCCGA

Figure 2-3

2581 GCTGCCTGCTGAAAGAGTGGACAGGGCTCCATGATGCTTTCGTTGAGACTGAGGACTTTA
-----+-----+-----+-----+-----+ 2640
CGACGGACGACTTCTCACCTGTCCCGAGGTACTACGAAAGCAACTCTGACTCCTGAAAT

2641 AGGTGAGAGACTGTTCCCACTCCACACTTGTTCAGTCTTCTGTCTCTTAGCAT
-----+-----+-----+-----+-----+ 2700
TCCACTCTCTGACAAAGGGTGGTTGAGGTGTGAACAAGGTCAGAAGGACAGAGAATCGTA

2701 CCTAGCCACCTGTTTCCCTAGGGCTCTGATGATGGCTGTACCATGGTACCCAAGAACTGC
-----+-----+-----+-----+-----+ 2760
GGATCGGTGGACAAAGGGATCCCGAGACTACTACCGACATGGTACCATGGGTCTTGACG

E VIII

2761 TACGTCAGCCAGCAGGACCTGGGACCGTTTCCGTCTGGTATCCGGATTGATTACGTGCTT
-----+-----+-----+-----+-----+ 2820
ATGCAGTCGGTCGTCTGGACCTGGCAAAGGCAGACCATAGGCCTAACTAATGCACGAA

2821 TACAAGGTCAGGCTCTTATTCGCGTGTGCCTTCTCCAGTATCTTCTTCTCTGTCACT
-----+-----+-----+-----+-----+ 2880
ATGTTCCAGTCCGAGAATAAGGGCCACACGGAAGAGGTCATAGAAGGAAGGAGACAGTGA

2881 AGCCACGCTTTAGTTCAGCTACAGTCTTGGGCCACTGATGGCTAAAGAATAGAATCCTG
-----+-----+-----+-----+-----+ 2940
TCGGGTGCGAAATCAAGTCGATGTCAAAACCGGTGACTACCGATTCTTATCTTAGGAC

2941 TCGGCTGCTTCTCTGGGAGAATTTAAGCTTCTCCATGTTCTTGCTCTTCTTAGGCAGTCT
-----+-----+-----+-----+-----+ 3000
AGCCGACCAAGAGACCCTCTTAAATTCGAAGAGGTACAAGAACGAGAAGGATCCGTCAGA

3001 CTGAGTTCCAGTCTGCTGTGAGACTCTGAAAACCACTACAGGCTGTGACCTCACAGTG
-----+-----+-----+-----+-----+ 3060
GACTCAAGGTGCAGACGACACTCTGAGACTTTTGGTGATGTCCGACACTGGGAGTGTAC

E IX

3061 ACAAGCCCTTCTCTGATCACGAGGCCCTCATGGCTACTTTGTATGTGAAGCACAGCCCCC
-----+-----+-----+-----+-----+ 3120
TGTTCCGGGAAGAGACTAGTGCTCCGGGAGTACCGATGAAACATACACTTCGTGTCCGGGG

3121 CTCAGGAAGACCCCTGTACTGCCTGTGGTAAGCAGCATTTCCTTTGCCCCCTCTACTTTA
-----+-----+-----+-----+-----+ 3180
GAGTCCTTCTGGGGACATGACGGACACCATTCGTCTGTAAGGAAACGGGGGAGATGAAAT

3181 AGGCAGCCCCGCTCCATCCTGACCCTCCCTGCTCTACGTTCTCTCTTTTCCAGGCCC
-----+-----+-----+-----+-----+ 3240
TCCGTCCGGGCGGAGGTAGGACTGGGAGGGGACGAGATGCAAGAGAGAAAAGGTCCGGG

3241 ACTGGAAAGGTCCGATTGATCAGCGTGCTAAGGGAGGCCAGGACAGAGCTGGGGCTAGG
-----+-----+-----+-----+-----+ 3300
TGACCTTTCCAGGCTAAACTAGTCGCACGATTCCCTCCGGTCCTGTCTCGACCCCGATCC

E X

3301 CATAGCTAAAGCTCGCTGGTGGGCTGCATTCTCTGGCTATGTGATCGTTTGGGGGCTGTC
-----+-----+-----+-----+-----+ 3360
GTATCGATTTCGAGCGACACCCGACGTAAGAGACCGATACACTAGCAAACCCCGACAG

3361 CCTTCTGGTGTGCTGTGTCTGCTGGCTGCAGGAGAAAGAGGCCAGGGAAGTGGCCATCAT
-----+-----+-----+-----+-----+ 3420
GGAAGACCACAACGACACACAGGACCGACGCTCTTCTCCGGTCCCTTCACCGGTAGTA

Figure 2-4

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CCTCTGCATACCCAGTGTGGGTCTGGTGTGGTAGCAGGTGCAGTCTACCTCTTCCACAA
3421 -----+-----+-----+-----+-----+ 3480
GGAGACGTATGGGTACACCCAGACCAGACCATCGTCCACGTGAGATGGAGAAGGTGTT

GCAGGAGGCCAAGGGCTTATGTCGGGGCCAGGCTGAGATGCTGCACGTTCTGACAAGGGA
3481 -----+-----+-----+-----+-----+ 3540
CGTCCTCCGGTTCCCGAATACAGCCCGGGTCCGACTCTACGACGTGCAAGACTGTTCCCT

AACGGAGACCCAGGACCCAGGCTCAGAGCCTCACCTAGCCTACTGCTTGACAGCAGGAGGG
3541 -----+-----+-----+-----+-----+ 3600
TTGCCTCTGGGTCTGGCTCCGAGTCTCGGAGTGGATCGGATGACGAACGTGCTCCTCCC
stop
GGACAGAGCTTAAAGAGCTTAACAATAAACTTGCTTGACACACTCTAGTGGCTCTACCTT
3601 -----+-----+-----+-----+-----+ 3660
CCTGTCTCGAATTCTCGAATTGTTATTTGAACGAAGTGTGTGAGATCACCGAGATGGAA

GTTCTTGCAGAGGCATGATGGGAAGTGAAGGTGAGTGGCCTTGTCACTGTGTGGCTTTA
3661 -----+-----+-----+-----+-----+ 3720
CAAGGAACGTCTCCGTACTACCCTTGACTTCCAGTCACCGGAACAGTGACACACCGAAAT

GAGCGTTGGCCTCTCACTTGCCCTTTTTCACACTCCCGTCTCCTGCCAGCACAGAGCAT
3721 -----+-----+-----+-----+-----+ 3780
CTCGCAACCGGAGAGTGAACGGAAAAACGTGTGAGGGCAGAGGACGGTCGTGTCTCGTA

AAACCCTGTTTCATGGTCATAATCCTTTTATTGTAAACAACGAAGCCTCTGACTAAGCAGT
3781 -----+-----+-----+-----+-----+ 3840
TTTGGGACAAGTACCAGTATTAGGAAAAATAACATTTGTGCTTCGGAGACTGATTCTGTC

CCAGATGGCGGAGGTACAGCCCTTGTGATGGTGTCTTGCTTACGGGGCAGGGAGGCAGCT
3841 -----+-----+-----+-----+-----+ 3900
GGTCTACCGCCTCCATGTCGGGAACACTACCACAGAACGAATGCCCCGTCCCTCCGTCGA

AACCATCATCTTCTAGCCCTGGGCTCCCATCTATGCAGGCATCTCTCTGAGCCTCCGTTCT
3901 -----+-----+-----+-----+-----+ 3960
TTGGTAGTAGAAGATCGGGACCCGAGGGTAGATACGTCGTTAGAGAGACTCGGAGGCAAG

CTCCTGGAATTGGNTCAGAGCAATCCCGCTTGGTTACCAACCTCCAAACAGCTTCCCTTA
3961 -----+-----+-----+-----+-----+ 4020
GAGGACCTTAACCNAGTCTCGTTAGGGCGAACCAAGTGGTTGGAGGTTTGTGGAAGGAAT

AGGACCTGGTTTCTCAAAANGGNAAGGTNCGGGCCTCCGGTCTTCAATANGTTTCTCTAA
4021 -----+-----+-----+-----+-----+ 4080
TCCTGGACCAAAGAGTTTNCNTTCCANGCCCGAGGCCAGAGTTATNCAAAGGATT

AAAGGGANGAATGAAAANCCTTAAGNNCCAACAAGGGGAACCCCTTGGNCCCAAAAGGGGA
4081 -----+-----+-----+-----+-----+ 4140
TTTCCCTNCTTACTTTTNGGAATTCNNGGTGTTCCTTGGGAACCNNGGTTTCCCTT

CCTGGGTGGTTTCCNTTGGGGCCAAANTTATCCCAAAGGGTCCAATTGAAGGGTTAAC
4141 -----+-----+-----+-----+-----+ 4200
GGACCCACCAAAGGGNAACCCCGGTTTNAATAGGGTTTCCCCAGGTTAACTTCCCAATTG

CCCCCAAAAANNACCGNTTTCCTCCCGGAATTTCCAAAGGTTTNNCCCCCCCCGGCAAAANC
4201 -----+-----+-----+-----+-----+ 4260
GGGGGTTTTTNNNTGGGNAAGGGGGCCTTAAAGGTTTCCAAANGGGGGGGCCGTTTTNG

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Figure 2-5

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TCCCTTGGGGNCCNAANCCNTGGCCCGGNCCTGGCTTTTCCCCCTTTCCCAAGNATTC
4261 -----+-----+-----+-----+-----+ 4320
AGGGAACCCCNNGGNTTNGGNACCGGGCCNGAACCGAAAAGGGGAAAGGGTTCNTAAAG

AAANNTTCCCTNGGAAANCCCTTGNTTGGNAAAACCNAATNANGAACCAANGCCAANNNT
4321 -----+-----+-----+-----+-----+ 4380
TTTNNAAAGGGANCTTTTNGGGGAACNAACCNTTTTGGNTTANTNCTTGGTNCGGTNNNA

TGCCAANAAACCNTTTGGGCAAAGGGGGNAAATTCANCAANGGGGNAATTGGGGAAACCC
4381 -----+-----+-----+-----+-----+ 4440
ACGGTTNTTTGGNAAACCCGTTTCCCCNTTTAAGTNGTTNCCCCNTTAACCCCTTTGGG

NTGGGTTTNCCCAAAGGGCCCNAAANANT
4441 -----+-----+-----+-----+-----+ 4468
NACCCAAANGGGTTTCCCGGGNTTNTNA
```

Figure 2-6

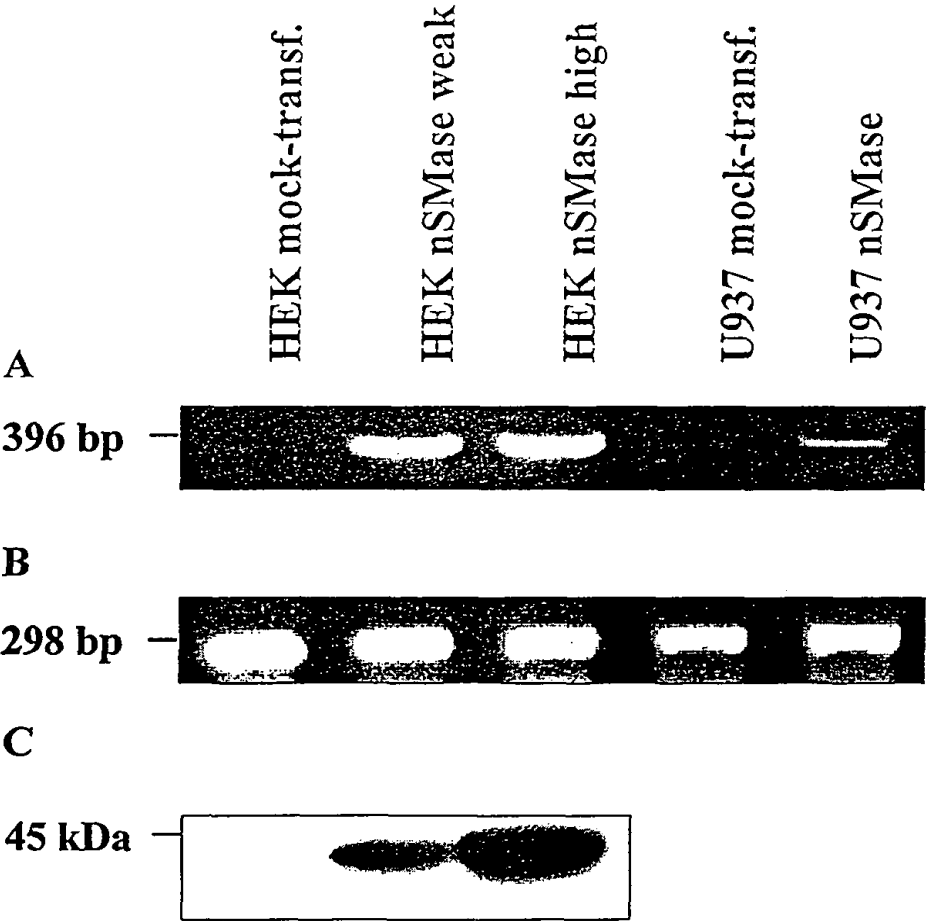


Figure 3

mnSMase "konventional" Knock Out

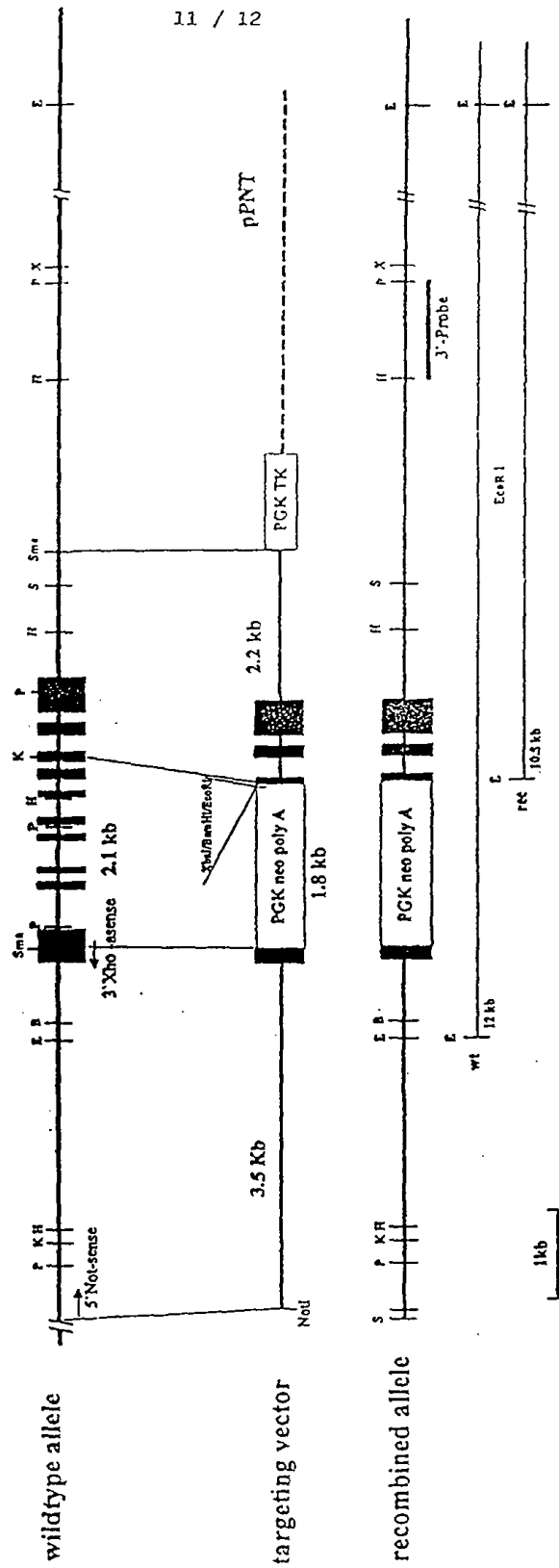


Figure 4

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Constructs for generating transgenic mouse mutants

ubiquitin promoter	nSMase	IRES	lacZ	polyA
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polyA	rtTA	CMV	CMV-1	nSMase	IRES	GFP	polyA
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Ubiquitin promoter: regulatory sequence of the ubiquitin gene, controlling a ubiquitous transcription.

nSMase: neutral sphingomyelinase

lacZ: lacZ, gene coding for β -galactosidase

polyA: recognition signal for the termination of transcription and polyadenylation

CMV: cytomegalovirus promoter of the cytomegalovirus gene, controlling a ubiquitous transcription.

rtTA: reverse transactivator, binds to the minimal promoter and thus controls transcription. The binding properties of the transactivator are influenced by tetracyclin. The addition of tetracyclin makes the transactivator bind to the minimal promoter and starts transcription, removal of tetracyclin prevents the binding of the transactivator to the minimal promoter and prevents transcription.

CMV-1: minimal promoter, binding of transactivator starts transcription.

IRES: *internal ribosomal entry sequence*, viral initiation signal for translation.

Figure 5